

~~ff~~ Bio-informatics  $\Rightarrow$  02-08-22

~~Amulya~~

# Cell  $\rightarrow$  ~~Cell Biology~~

- All living organisms are composed of one or more cell.
- The cell is the basic unit of structure and organization in organism.
- Cell arise from pre-existing cells
- Cell theory Robert Hooke - 1665
- Brief theory of cell: Matthias Schleiden and Theodor Schwann - 1839.

# Type of cell.

- Based on nucleus.
  - Prokaryotic
  - Eukaryotic
- Based on physical structure
  - somatic cell
  - $\rightarrow$  Mitosis cell division
  - $\rightarrow$  Gamete
  - Meiosis cell division

- Based on number of chromosomes in nucleus
- Diploid cell → two homologous sets
- Haploid cell → one set

## Report.

Wings. Bright yellow with black markings.  
(Lob. N. 2226 No. 5143) 

~~get out things  
off - not to~~

anglophile and Anglophilic countries / Anglophil  
The old is not always better

A simple line drawing of a tree. It features a vertical stem on the left and a large, roughly circular canopy on top. A small, irregular circle representing the trunk is positioned near the bottom center of the canopy.

200

## cell organelles

→ Ribosome R

→ antibody

 Healthcare → Lysisome

**Healthcare**

- Golgi body
- Lysosome
- Endoplasmic reticulum (smooth & rough)

levocetirizine tablet & solution



## Plasma membrane → outer boundary.

- Biological membrane is on outer membrane of the cell.
- Composed of two larger phospholipid molecules (Fluid Mosaic Model)
- Plasma membrane regulates the entry and exit of cell.
- Plasma membrane surrounds the cytoplasm and constituents of the cell.

## Nucleus

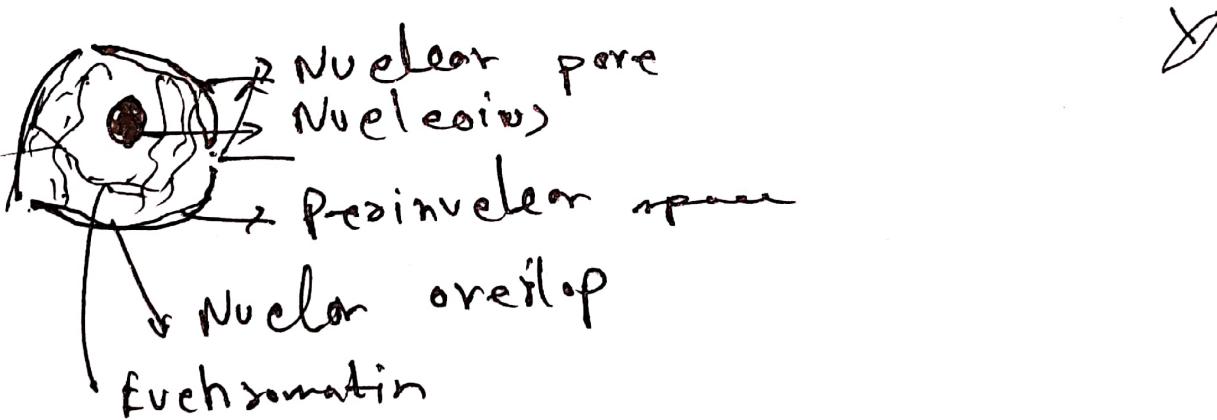
- Double layered structure encloses the nucleus is connected to the ER.
- Perinuclear space.
- The nucleus communicates with the remaining of the cell or the cytoplasm through several openings, called nuclear pores.

## # ~~Chromosomes~~ chromosomes

→ chromosome are present in the form of strings of DNA and histones (protein molecule) called chromatin again classified into heterochromatin & euchromatin.

## # Nucleus:

The nucleolus plays an indirect role in protein synthesis by producing ribosomes. These ribosomes are cell organelles made up of RNA and proteins... ~~present in the~~.



# 06.08.22

# Bio-Informatics Lection 1

- go over all chromatin are involved in

## # Chromatin

↓ content the DNA to split  
↓ heterochromatin & euchromatin

### Heterochromatin

### Euchromatin

- not carry any type of genetic material.
  - inactive on reproduction system
  - can't cross over.
- carry any type of genetic material
- active on reproduction system
- Crossing over.

# The concept

## # Introduction to DNA

- one class of macromolecules contained in chromatin are called nucleic acid.

Early 20th century research into the identity of nucleic acids culminated with the conclusion that nucleic acids are polymers, or repeating chains

of smaller, similarly structured molecules known as monomers. Because of their tendency to be long and thin, nucleic acid polymers are commonly known as strands.

The nucleic acid monomer is called nucleotide and is used as a unit of strand length. Each nucleotide is formed of three parts:

- a sugar molecule
- a negatively ion charged molecule called a phosphate, and a
- a compound called a nucleobase.

Polymerization achieved as the sugar of one nucleotide bonds to the phosphate of the next nucleotide in the chain which forms a sugar-phosphate backbone for the nucleic acid strand.

# strand: word meaning of many  
long chains of joined sub-unit  
→ strand is the commonly used term  
for a polymer of nucleic acid. RNA  
contains single strand, whereas DNA  
contains two strands linked together  
by base pair bonding and twisted  
around into a double helix shape.

[HW]

→ Ribose

→ Deoxyribose

→ Cross-over

{ next class

Central dogma:

# 13.08.22

Saturday

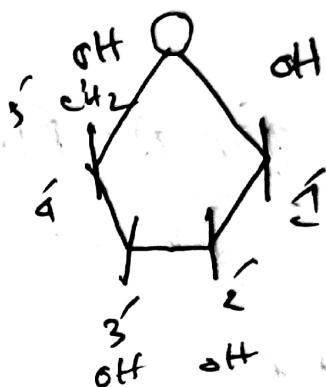
## # Introduction to DNA

Nucleic acid has two sugars -

### ① Deoxyribose



### ② Ribose



- Deoxyribose nucleic acid (DNA)
- only four choices for nucleobases arise molecules are called
  - Adenine (A) - Purine
  - Cytosine (C) - Pyrimidine
  - Guanine (G) - Purine
  - Thymine (T) - Pyrimidine
- The total number of DNA is known as genome.

- ribose nucleic acid (RNA)
- structure is similar to DNA. However, it difference from DNA by uracil (U) in place of thymine (T).
  - The nucleotides for RNA are -
    - Adenine (A)
    - Cytosine (C)

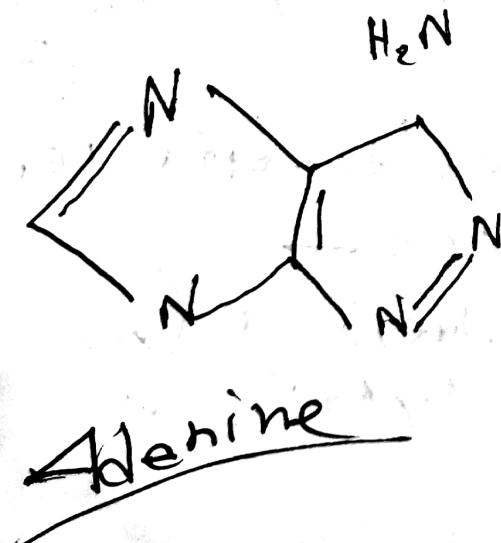
- Guanine (g)  
- Uracil (u)

# Diff DNA - RNA  
Double Helix

Adenine / Thymine  
Structure

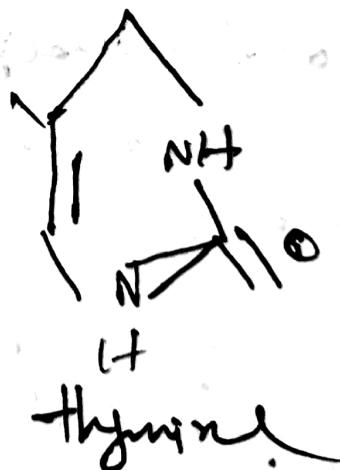
## Purine

- Adenine is a nucleobase with a double-ring structure. Purine comprise adenine and guanine.



## Pyrimidine

- Pyrimidine are nucleobase with single-ring structures. Pyrimidine comprise cytosine, thymine, or uracil.



## Biological information:

-DNA sequence

ATGTAATGGATCG-----

-RNA

ATCUATCUU-----

— — —

## Homework

- ① DNA & RNA → Difference
- ② Animal Cell → Difference
- ③ Purine & Pyrimidine Difference
- ④ DNA and RNA structures
- ⑤ DNA Double Helix Structure

## Next class:

- central dogma
- genome code.

## # Central Dogma

The central Dogma is the process by which the instruction in DNA are converted into a functional Product.

It was first proposed in 1958 by Francis Crick, discover of the structure of DNA.

In other words, it is a flow of genetic information from DNA to RNA, to make a functional product a protein.

The central dogma suggests that DNA contains the information needed to make all of our proteins and that RNA is a messenger (mRNA) that carries this information to the ribosome.

The process by which the DNA instruction are converted into the functional product is called gene expression.

# Gene Expression has 2 stages, Date 16-08-22  
Page

# Transcription: The information in the DNA of every cell is converted into small, portable RNA message.

DNA  $\xrightarrow{\text{transcription}}$  RNA

# Transcription: During translation, these messages travel from where the DNA is the cell nucleus to the ribosome where they are "read" to make specific proteins.

RNA  $\xrightarrow{\text{translation}}$  Protein.

# Reverse Transcription: retrovirus  
of HIV

# Homework

① Reverse Transcription

# next class:

Codon  $\rightarrow$  Protein

↓  
Genetic Codon.

23.08.22

## # Lecture-5

Date \_\_\_\_\_

Page \_\_\_\_\_

→ Sequence Alignment

→ Lab sequence (LS) → found sequence  
↳ Reference Sequence (RS)  
↳ original sequence

# Sequence Alignment is the process of comparing and detecting similarities between biological sequences.

We have two types of sequence:

Lab sequence, the reference sequence  
You can get from a lab during experiment.

Reference Sequence - a standard of original sequence that you want to match/compose with (LS)

### Sequence Alignment

Pairwise Alignment

- used to identify regions of similarity that may include functional, structural and/or evolutionary relationships between two biological sequences.

Multiple Alignment  
is the alignment of these or more biological sequences of similar length.

## Alignment Score

Date \_\_\_\_\_

Page \_\_\_\_\_

↳ Highest numbers of sequence between two.

Alignment score: the value that measures the degree of sequence similarity is called alignment sequence.

# Pairwise, two types:

→ Local Alignment

Local Alignment

Global Alignment

- find local regions with the process that is used to find the matching of similarity and whole/entire sequence is align them.

- Algorithm: Smith - waterman Algorithm

- Algorithm: needleman - wanisch algorithm.

Example:

$$LS = \dots A \underset{\text{C}}{\underset{\text{G}}{\underset{\text{T}}{|}}} \dots$$

$$RS = AACACGTTGTCT$$

$$LS = A \underset{\text{C}}{\underset{\text{G}}{\underset{\text{T}}{|}}} \dots G T \dots \dots$$

$$RS = AACAG \underset{\text{C}}{\underset{\text{G}}{\underset{\text{T}}{|}}} TG T C T$$

①

$$LS = A \underset{\text{C}}{\underset{\text{G}}{\underset{\text{T}}{|}}} \dots G \dots T$$

$$RS = AACACGTTGTCT$$

# Smitwaster Mon

Date \_\_\_\_\_

Parameter

Algorithm

Page \_\_\_\_\_

match  $\equiv \rightarrow 1$

mismatch  $\equiv 0$

gap  $\equiv 0.1$

Dynamic

Algorithm

① Gap

Edit

② match

Distance.

nucleotides

$$\text{identity}(LS, RS) = \frac{\text{numbers of match identical}}{\min(\text{Length}(LS), \text{Length}(RS))} \times 100\%$$

$$\text{identity}(TS, B) = \frac{9}{\min(9, 11)} \times 100\%$$

$$= \frac{9}{9} \times 100\%$$

$$= 100\%$$

It.

## #Needeman-Wunsek Algorithm for global alignment.

Page

steps:

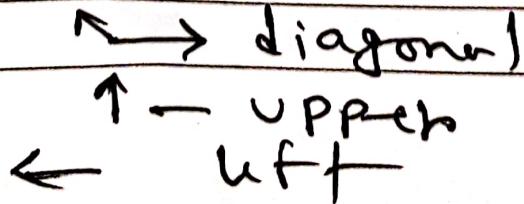
1. Add a gap penalty to all cells
2. for a particular cell, (initialization)
  - i) horizontally (left adjacent)
  - ii) vertically (upper adjacent)

(2) Now, considering the the diagonal checking, check whether ~~match~~ the nucleotides match or mismatch.

(iii) add the value of match or mismatch with the immediate diagonal cell.

(3) find maximum among (i), (ii), and (iii) for the cell.

(4) for each calculation mark with an arrow from which you have found the maximum value. the arrows might have



$$\textcircled{5} \quad \begin{array}{|c|c|} \hline 1 & 0 \\ \hline -3 & 5 \\ \hline \end{array} \quad \begin{array}{|c|c|} \hline 3 & 0 \\ \hline -3 & 2 \\ \hline \end{array}$$

Exactly matched      mismatch

$$\begin{array}{|c|c|} \hline -3 & 0 \\ \hline 3 & 5 \\ \hline \end{array} \quad \text{or} \quad \begin{array}{|c|c|} \hline 3 & 0 \\ \hline 3 & 5 \\ \hline \end{array} \quad \left. \begin{array}{l} \text{group} \\ \text{group} \end{array} \right\}$$

(1,3) matrix filling  
 (9,5) trace back

	A	T	G	C	T	
A	0	-2	-9	-8	-8	-10
G	-2	↑ 1	← -1	← -3	← -5	← -7
C	-9	-1↑	↑ 0	↑ 0	← -2	← -1
T	-6	-3↑	-2↑	-1↑	1↑	-1
	-8	↑ -5↑	↑ -2	↑ -3	↑ -1↑	↑ 2

3 Trace back

$$\begin{array}{l} \text{A T G C T} \\ \text{A - G C T} \end{array} \quad \left. \begin{array}{l} \text{Match} \\ \text{Match} \end{array} \right\}$$

Perform local alignment by applying Smith-waterman algorithm on the following sequences:-

$$RS = AGCGTAG$$

$$LS = CTCGTC$$

Here,  
Match = +1  
Mismatch = -1  
Gap = -2

	A	G	C	G	T	A	G
O	0	0	0	0	0	0	0
C	0	0	0	1	0	0	0
T	0	0	0	0	0	1	0
C	0	0	0	0	0	0	0
G	0	0	1	0	0	0	1
T	0	0	0	0	0	0	0
C	0	0	0	1	0	0	0

Alignment Score: 3

Local Alignmt = CGT